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SEQUENCE LISTING

TECH CENTER 1600/2900

JAN 10 2002

RECEIVED

(1) GENERAL INFORMATION:

- (i) APPLICANT: Nelson, Edward L.
Nelson, Peter J.
- (ii) TITLE OF INVENTION: NOVEL VECTOR FOR
POLYNUCLEOTIDE VACCINES
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 - (B) STREET: 345 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/14306
 - (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US60/023931
 - (B) FILING DATE: 14-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: KATHRYN M. BROWN
 - (B) REGISTRATION NUMBER: 34556
 - (C) REFERENCE/DOCKET NUMBER: 2026-4236US1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 758-4800
 - (B) TELEFAX: (212) 751-6849
 - (C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:1:

GGCCGCGTTG	CTGGCGTTTT	TCCATAGGCT	CCGCCCCCCT	40
GACGAGCATC	ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC	80
GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTTCCCCC	120
TGGAAGCTCC	CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	160
CTTACCGGAT	ACCTCTCCGC	CTTTCTCCCT	TCGGGAAGCG	200
TGGCGCTTTC	TCAATGCTCA	CGCTGTAGGT	ATCTCAGTTC	240
GGTGTAGGTC	GTTGCGTCCA	AGCTGGGCTG	TGTGCACGAA	280
CCCCCGTTC	AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	320
ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	360
ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	400
TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	440
ACTACGGCTA	CAC			453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:2:

GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG	40
CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCACT	80
GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	120
GACTCAAGAC	GATAGTTACC	GGATAAGGCG	CAGCGGTCGG	160
GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	GCTTGGAGCG	200
AACGACCTAC	ACCGAACTGA	GATACCTACA	CCGTGAGCAT	240
TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	AAGGCGGACA	280
GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	320
GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	360
CCTGTCCGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT	400
TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	440
CAGCAACGCG	GCC			453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

GAATTCTTTC	GGACTTTTGA	AAGTGATGGT	GGTGGCCGAA	40
GGATTCGAAC	CTTCGAAGTC	GATGACGGCA	GATTAGAGT	80
CTGCTCCCTT	TGGCCGCTCG	GGAACCCAC	CACGGGTAAT	120
GCTTTTACTG	GCCTGCTCCC	TTATCGGGAA	GCGGGGCGCA	160
TCATATCAAA	TGACGCGCCG	CTGTAAAGTG	TTACGTTGAG	200
AAAGAATTC				209

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

GAATTCTTTC	TCAACGTAAC	ACTTTACAGC	GGCGCGTCAT	40
TTGATATGAT	GCGCCCCGCT	TCCCGATAAG	GGAGCAGGCC	80
AGTAAAAGCA	TTACCCGTGG	TGGGGTTCCC	GAGCGGCCAA	120
AGGGAGCAGA	CTCTAAATCT	GCCGTCATCG	ACTTCGAAGG	160
TTCGAATCCT	TCCCCCACCA	CCATCACTTT	CAAAAGTCCG	200
AAAGAATTC				209

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:5:

AATAAA

6

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:6:

ATTAAA

6

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

AGTAAA

6

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

AAGAAC

6

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

AATACA

6

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

GCCTTAAGGG	CCATATGGTG	AGTGGATCCC	TTGACCCCAG	40
GCGGGGATGG	GGAGACCTGT	AGTCAGAGCC	CCCGGGCAGC	80
ACAGGCCAAT	GCCCGTCCTT	CCCCTGCAGG	ATGAGTAGTG	120
AGTGCCCTCTC	CTGGCCCTGG	AAGTTGCCAC	TCCAGTGCCC	160
ACCAGCCTTG	TCCTAATAAA	ATTAAGTTGC	ATCATTTTGT	200
CTGACTAGGT	GTCCTCTATA	ATATTAT		227

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

ATAATATTAT	AGAGGACACC	TAGTCAGAAC	AAATGATGCA	40
ACTTAATTTT	ATTAGGACAA	GGCTGGTGGG	CACTGGAGTG	80
GCAACTTCCA	GGGCCAGGAG	AGGCACTCAC	TACTCATCCT	120
GCAGGGGAAG	GACGGGCATT	GGCCTGTGCT	GCCCGGGGGC	160
TCTGACTACA	GGTCTCCCCC	ATCCCCGCCT	GGGGTCAAGG	200
CATCCACTCA	CCATATGGCC	CTTAAGG		227

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

CCTCGGTACC	TGCCATGGCG	CGGATTCTTT	ATCACTGATA	40
AGTTGGTGGA	CATATTATGT	TTATCAGTGA	TAAAGTGTCA	80
AGCATGACAA	AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	120
GCCCTGGACT	GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	160
GACACGCAAA	CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	200
GCGCTTTACT	GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	240
GGCCATATGC	CG			252

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

CCTCGGTACC TGCCACCATG GCGCGGATTC TTTAT

35

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

CGGCATATGG CCTTAAGGCG CCCGCTTGTT CCTGAAGT

38

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

GCCTTAAGGG CCATATGGTG AGTGGATGCC TTGACCCCAG
GCGGGGATGG GGGAGACCTG TAGTCAGAGC CCCCGGGCAG

40

80

CACAGGCCAA TGCCCGTCCT TCCCCTGCAG GATGAGTAGT
GAGTGCCTCT CCTGGCCCTG GAAGTTGCCA CTCCAGTGCC
CACCAGCCTT GTCCTAATAA AATTAAGTTG CATCATTTTG
TCTGACTAGG TGTCTCTAT AATATTAT

120

160

200

228

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCCATGGCG	CGGATTCTTT	ATCACTGATA	AGTTGGTGGGA	40
CATATTATGT	TTATCAGTGA	TAAAGTGTC	AGCATGACAA	80
AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	GCCCTGGACT	120
GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	GACACGCAAA	160
CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	GCGCTTTACT	200
GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	GGCCATATGG	240
TGAGTGGATG	CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	280
TGTAGTCAGA	GCCCCCGGGC	AGCACAGGCC	AATGCCCGTC	320
CTTCCCCCTG	AGTGAGTAGT	GACTGCCCCG	GTGGGATCCC	360
TGTGACCCCT	CCCCAGTGCC	TCTCCTGGCC	CTGGAAGTTG	400
CCACTCCAGT	CCCCACCAGC	CTTGTCTTAA	TAAAATTAAG	440
TTGCATCATT	TTGTCTGACT	AGGTGTCCTC	TATAATATTA	480
TAAGCTTGAT	ATCGAATTCT	TTCTCAACGT	AACACTTTAC	520
AGCGGCGCGT	CATTTGATAT	GATGCGCCCC	GCTTCCCGAT	560
AAGGGAGCAG	GCCAGTAAAA	GCATTACCCG	TGGTGGGGTT	600
CCCGAGCGGC	CAAAGGGAGC	AGACTCTAAA	TCTGCCGTCA	640
TCGACTTCGA	AGGTTCTGAAT	CCTTCCCCCA	CCACCATCAC	680
TTTCAAAAGT	CCGAAAGAAT	TCCTGCAGCC	CGTGTAGCCG	720
TAGTTAGGCC	ACCACTTCAA	GAACCTCTGT	GCACCGCCTA	760
CATACCTCGC	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	800
CAGTGGCGAT	AAGTCGTGTC	TTACCGGGTT	GGACTCAAGA	840
CGATAGTTAC	CGGATAAGGC	GCAGCGGTCT	GGCTGAACGG	880
GGGGTTTCGT	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	920
CACCGAACTG	AGATACCTAC	AGCGTGAGCA	TTGAGAAAGC	960
GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	1000
TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	1040
TCCAGGGGGA	AACGCCTGGT	ATCTTTATAG	TCCTGTCGGG	1080
TTTCGCCACC	TCTGACTTGA	GCGTCGATTT	TTGTGATGCT	1120
CGTCAGGGGG	GCGGAGCCTA	TGGAAAAACG	CCAGCAACGC	1160
GGCCGGGGGA	TCCGGAGAGC	TCACTCTAGA	TGAGAGAGCA	1200
GTGAGGGAGA	GACAGAGACT	CGAATTTCCG	GAGCTATTTC	1240
AGTTTTCTTT	TCCGTTTTGT	GCAATTTTAC	TTATGATACC	1280
GGCCAATGCT	TGGTTGCTAT	TTTGAAACT	CCCCTTAGGG	1320
GATGCCCTC	AACTGGCCCT	ATAAGGGCC	AGCCTGAGCT	1360
GCAGAGGATT	CCTGCAGAGG	ATCAAGACAG	CACGTGGACC	1400
TGCACAGCC	TCTCCACAG	GTACC		1425

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

ATGAGCAAGG	GCGAGGAACT	GTTCACTGGC	GTGGTCCCAA	40
TTCTCGTGGA	ACTGGATGGC	GATGTGAATG	GGCACAAATT	80
TTCTGTCAGC	GGAGAGGGTG	AAGGTGATGC	CACATACGGA	120
AAGCTCACCC	TGAAATTTCAT	CTGCACCACT	GGAAAGCTCC	160
CTGTGCCATG	GCCAACACTG	GTCACTACCT	TCACCTATGG	200
CGTGCAGTGC	TTTTCCAGAT	ACCCAGACCA	TATGAACGAG	240
CATGACTTTT	TCAAGAGCGC	CATGCCCCGAG	GGCTATGTGC	280
AGGAGAGAAC	CATCTTTTTT	AAAGATGACG	GGAACATAAA	320
GACCCGCGCT	GAAGTCAAGT	TCGAAGGTGA	CACCCTGGTG	360
AATAGAATCG	AGTTGAAGGG	CATTGACTTT	AAGGAAGATG	400
GAAACATTCT	CGGCCACAAG	CTGGAATACA	ACTATAACTC	440
CCACAATGTG	TACATCATGG	CCGACAAGCA	AAAGAATGGC	480
ATCAAGGTCA	ACTTCAAGAT	CAGACACAAC	ATTGAGGATG	520
GATCCGTGCA	GCTGGCCGAC	CATTATCAAC	AGAACACTCC	560
AATCGGCGAC	CGCCCTGTGC	TCCTCCCAGA	CAACAATTAC	600
CTGTCCACCC	AGTCTGCCCT	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGACCA	CATGGTCCTG	CTGGAGTTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGC	719

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:

TATGAGCAAG	GGCGAGGAAC	TGTTCACTGG	CGTGGTCCCA	40
ATTCTCGTGG	AACTGGATGG	CGATGTGAAT	GGGCACAAAT	80
TTTCTGTCAG	CGGAGAGGGT	GAAGGTGATG	CCACATACGG	120
AAAGCTCACC	CTGAAATTCA	TCTGCACCAC	TGGAAAGCTC	160
CCTGTGCCAT	GGCCAACACT	GGTCACTACC	TTCACCTATG	200
GCGTGACGTG	CTTTTCCAGA	TACCCAGACC	ATATGAAGCA	240
GCATGACTTT	TTCAAGAGCG	CCATGCCCGA	GGGCTATGTG	280
CAGGAGAGAA	CCATCTTTTT	CAAAGATGAC	GGGAAC TACA	320
AGACCCGCGC	TGAAGTCAAG	TTCGAAGGTG	ACACCCTGGT	360
GAATAGAATC	GAGTTGAAGG	GCATTGACTT	TAAGGAAGAT	400
GGAAACATTC	TCGGCCACAA	GCTGGAATAC	AACTATAACT	440
CCCACAATGT	GTACATCATG	GCCGACAAGC	AAAAGAATGG	480
CATCAAGGTC	AACTTCAAGA	TCAGACACAA	CATTGAGGAT	520
GGATCCGTGC	AGCTGGCCGA	CCATTATCAA	CAGAACA CT C	560
CAATCGGCGA	CGGCCCTGTG	CTCCTCCCAG	ACAACCATTA	600
CCTGTCCACC	CAGTCTGCCC	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGACCA	CATGGTCCCTG	CTGGAGTTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGCC	720
ATATGGTGAG	TGGATGCCTT	GACCCCAGGC	GGGGATGGGG	760
GAGACCTGTA	GTCAGAGCCC	CCGGGCAGCA	CAGGCCAATG	800
CCCGTCCTTC	CCCTGCAGTG	AGTAGTGACT	GCCCCGGGTG	840
GATCCCTGTG	ACCCCTCCCC	AGTGCCTCTC	CTGGCCCTGG	880
AAGTTGCCAC	TCCAGTGCCC	ACCAGCCTTG	TCCTAATAAA	920
ATTAAGTTGC	ATCATTTTGT	CTGACTAGGT	GTCCTCTATA	960
ATATTATAAG	CTTGATATCG	AATTCTTTCT	CAACGTAACA	1000
CTTTACAGCG	GCGCGTCATT	TGATATGATG	CGCCCCGCTT	1040
CCCGATAAGG	GAGCAGGCCA	GTAAAAGCAT	TACCCGTGGT	1080
GGGGTTCCCG	AGCGGCCAAA	GGGAGCAGAC	TCTAAATCTG	1120
CCGTCAATCGA	CTTCGAAGGT	TCGAATCCTT	CCCCCACCAC	1160
CATCACTTTC	AAAAGTCCGA	AAGAATTCCT	CAGCCCCGTG	1200
TAGCCGTAGT	TAGGCCACCA	CTTCAAGAAC	TCTGTAGCAC	1240
CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC	1280
TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	1320
TCAAGACGAT	AGTTACCGGA	TAAGGCGCAG	CGGTCGGGCT	1360
GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	1400
GACCTACACC	GAAGTGAGAT	ACCTACAGCG	TGAGCATTGA	1440
GAAAGCGCCA	CGCTTCCCGA	AGGGAGAAAG	CGGGACAGGT	1480
ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG	1520
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	1560
GTCGGGTTTC	GCCACCTCTG	ACTTGAGCGT	CGATTTTTGT	1600
GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG	1640
CAACGCGGCC	GGGGGATCCG	GAGAGCTCAC	TCTAGATGAG	1680
AGAGCAGTGA	GGGAGAGACA	GAGACTCGAA	TTTCCGGAGC	1720
TATTTCAAGT	TTCTTTTCCG	TTTTGTGCAA	TTTCACTTAT	1760
GATACCGGCC	AATGCTTGGT	TGCTATTTTG	GAAACTCCCC	1800
TTAGGGGATG	CCCCTCAACT	GGCCCTATAA	AGGGCCAGCC	1840
TGAGCTGCAG	AGGATTCCCTG	CAGAGGATCA	AGACAGCACG	1880
TGGACCTCGC	ACAGCCTCTC	CCACAGGTAC	C	1911

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:19:

```

Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro
 1          5          10
Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn
          15          20
Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly
25          30          35
Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser
          40          45
Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
50          55          60
Val Leu Gly Val Val Phe Gly Ile Leu
          65

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:

```

Pro Ala Pro Gly Ala Gly Gly Met Val His His Arg
 1          5          10
His Arg Ser Ser Ser Thr Arg Ser Gly Gly Gly Asp
          15          20
Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala
25          30          35
Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly
          40          45
Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala
50          55          60
Ala Lys Gly Leu Ser Leu Pro Thr His Asp Pro Ser
          65          70
Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro
          75          80
Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
85          90          95

Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
          100          105
Asp Val Arg Pro Pro Pro Ser Pro Arg Glu Gly Pro
110          115          120

Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
          125          130
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val
135          140

```

Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu
145					150					155	
Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln	Gly	Thr	Cys	Ser
			160					165			
Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg
	170					175					180
Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro
				185					190		
Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro
		195					200				
Lys	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp
205					210					215	
Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu
			220					225			
Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro
	230					235					240
His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn
				245					250		
Leu	Tyr	Tyr	Trp	Asp	Asp	Pro	Pro	Glu	Arg	Gly	Ala
		255					260				
Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu
260					270					275	
Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Val	
			280					285			

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile	Ile	Ser	Ala	Val	Val	Gly	Ile	Leu	Leu	Val	Val
1				5					10		
Val	Leu	Gly	Val	Val	Phe	Gly	Ile	Leu	Ile		
		15					20				

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: No
 (iv) ANTI-SENSE: No
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:22:

GCCACCATGG	CCCCTGACCT	CTCCTACATG	CCCATCTGGA	40
AGTTTCCAGA	TGAGGAGGGC	GCATGCCAGC	CTTGCCCCAT	80
CAACTGCACC	CACTCCTGTG	TGGACCTGGA	TGACAAGGGC	120
TGCCCCGCCG	AGCAGAGAGC	CAGCCCTCTG	ACGTCCATCA	160
TCTCTGCGGT	GGTTGGCATT	CTGCTGGTCG	TGGTCTTGGG	200
GGTGGTCTTT	GGGATCCTCA	TCAAGCGACG	GCAGCAGAAG	240
ATCACATGTC	CAGACCCTGC	CCCGGGCGCT	GGGGGCATGG	280
TCCACCACAG	GCACCGCAGC	TCATCTACCA	GGAGTGGCGG	320
TGGGGACCTG	ACACTAGGGC	TGGAGCCCTC	TGAAGAGGAG	360
GCCCCCAGGT	CTCCACTGGC	ACCCTCCGAA	GGGGCTGGCT	400
CCGATGTATT	TGATGGTGAC	CTGGGAATGG	GGGCAGCCAA	440
GGGGCTGCAA	AGCCTCCCCA	CACATGACCC	CAGCCCTCTA	480
CAGCGGTACA	GTGAGGACCC	CACAGTACCC	CTGCCCTCTG	520
AGACTGATGG	CTACGTTGCC	CCCCTGACCT	GCAGCCCCCA	560
GCCTGAATAT	GTGAACCAGC	CAGATGTTCT	GCCCCAGCCC	600
CCTTCGCCCC	GAGAGGGCCC	TCTGCCTGCT	GCCCCGACCTG	640
CTGGTGCCAC	TCTGGAAAGG	CCCAAGACTC	TCTCCCCAGG	680
GAAGAATGGG	GTCGTCAAAG	ACGTTTTTGC	CTTTGGGGGT	720
GCCGTGGAGA	ACCCCGAGAC	TTGACACCCC	AGGGAGGAGC	760
TGCCCCCTCAG	CCCCACCCTC	CTCCTGCCTT	CAGCCCAGCC	800
TTCGACAACC	TCTATTACTG	GGACCAGGAC	CCACCAGAGC	840
GGGGGGCTCC	ACCCAGCACC	TTCAAAGGGA	CACCTACGGC	880
AGAGAACCCA	GAGTACCTGG	GTCTGGACGT	GCCAGTGTGA	920
AGCCTTAAGG	GCCATATGGT	GAGTGGATGC	TCTGACCCCA	960
GGCGGGGATG	GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	1000
GCACAGGCCA	ATGCCCCGTCC	TTCCCCTGCA	GTGAGTAGTG	1040
ACTGCCCCGG	TGGGATCCCT	GTGACCCCTC	CCCAGTGCCT	1080
CTCCTGGCCC	TGGAAGTTGC	CACTCCAGTG	CCCACCAGCC	1120
TTGTCCTAAT	AAAATTAAGT	TGCATCATTT	TGTCTGACTA	1160
GGTGTCTCT	ATAATATTAT	AAGCTTGATA	TCGAATTCTT	1200
TCTCAACGTA	ACACTTTACA	GCGGCGCGTC	ATTTGATATG	1240
ATGCGCCCCG	CTTCCCGATA	AGGGAGCAGG	CCAGTAAAAG	1280
CATTACCCGT	GGTGGGGTTC	CCGAGCGGCC	AAAGGGAGCA	1320
GACTCTAAAT	CTGCCGTCAT	CGACTTCGAA	GGTTCGAATC	1360
CTTCCCCCAC	CACCATCACT	TTCAAAGTTC	CGAAAGAATT	1400
CCTGCAGCCC	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1440
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	1480
TGTTACCACT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	1520
TACCGGGTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	1560
CAGCGGTCGG	GCTGAACGGG	GGGTTTCGTG	ACACAGCCCA	1600
GCTTGAGCG	AACGACCTAC	ACCGAACTGA	GATACCTACA	1640
GCGTGAGCAT	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	1680
AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	1720
GAGAGCGCAC	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	1760
TCTTTATAGT	CCTGTCGGGT	FTCGCCACCT	CTGACTTGAG	1800
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	1840
GGAAAAACGC	CAGCAACGCG	GCCGGGGGAT	CCGGAGAGCT	1880
CACCTTAGAT	GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	1920
GAATTTCCGG	AGCTATTTC	GTTTTCTTTT	CCGTTTTGTG	1960

CAATTTCACT	TATGATACCG	GCCAATGCTT	GGTTGCTATT	2000
TTGGAAACTC	CCCTTAGGGG	ATGCCCCTCA	ACTGGCCCTA	2040
TAAAGGGCCA	GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	2080
TCAAGACAGC	ACGTGGACCT	CGCACAGCCT	CTCCCACAGG	2120
TACCT				2125

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

GTCTGCCACC ATGGCCTACT CCCCTGC

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

TTCTTTGGTG ACCTACCTCT TCGGAATTGC CGAGTC

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	40
TGAGTCAGGA	AACATTTTCA	GACCTATGGA	AACTACTTCC	80
TGAAAACAAC	GTTCTGTCCC	CCTTGCCGTC	CCAAGCAATG	120
GATGATTTGA	TGCTGTCCCC	GGACGATATT	GAACAATGGT	160
TCACTGAAGA	CCCAGGTCCA	GATGAAGCTC	CCAGAATGCC	200
AGAGGCTGCT	CCCCGCGTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCGGCGG	CCCCTGCACC	AGCCCCCTCC	TGGCCCCCTGT	280
CATCTTCTGT	CCCTTCCCAG	AAAACCTACC	AGGGCAGCTA	320
CGGTTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGCCACCA	TGGCCTACTC	CCCTGCGTCT	GTGACTTGCA	400
CGTACTCCCC	TGCCCTCAAC	AAGATGTTTT	GCCAACTGGC	440
CAAGACTGTC	CCTGTGCAGC	TGTGGGTTGA	TTCCACACCC	480
CCGCCCCGCA	CCCGCGTCCG	CGCCATGGCC	ATCTACAAGC	520
AGTCACAGCA	CATGACGGAG	GTTGTGAGGC	GCTGCCCCCA	560
CCATGAGCGC	TGCTCAGATA	GCGATGGTCT	GGCCCCCTCCT	600
CAGCGTCTTA	TCCGAGTGGA	AGGAAATTTG	CGTGTGGAGT	640
ATTTGGATGA	CAGAAACACT	TTTCGACATA	GTGTGGTGGT	680
GCCCTATGAG	CCGCCTGAGG	TTGGCTCTGA	CTGTACCACC	720
ATCCACTACA	ACTACATGTG	TAACAGTTCC	TGCATGGGCG	760
GCATGAACCG	GAGGCCCATC	CTCACCATCA	TCACACTGGA	800
AGACTCCAGT	GGTAATCTAC	TGGGACGGAA	CAGCTTTGAG	840
GTGCGTGTTT	GTGCCTGTCC	TGGGAGAGAC	CGGCGCACAG	880
AGGAAGAGAA	TCTCCGCAAG	AAAGGGGAGC	CTCACCACGA	920
GCTGCCCCCA	GGGAGCACTA	AGCGAGCACT	GCCCAACAAC	960
ACCAGCTCCT	CTCCCCAGCC	AAAGAAGAAA	CCACTGGATG	1000
GAGAATATTT	CACCCTTCAG	ATCCGTGGGG	GTGAGCGCTT	1040
CGAGATGTTT	TTTGGTGACC	TACCTCTTCG	GAATTGCCGA	1080
GTCTTCCGAG	AGCTGAATGA	GGCCTTGGA	CTCAAGGATG	1120
CCCAGGCTGG	GAAGGAGCCA	GGGGGGAGCA	GGGCTCACTC	1160
CAGCCACCTG	AAGTCCAAAA	AGGGTCAGTC	TACCTCCCGC	1200
CATAAAAAAC	TCATGTTCAA	GACAGAAGGG	CCTGACTCAG	1240
AC				1242

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:26:

CTCGGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	40
CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	80
TGGCGAAACC	CGACAGGACT	ATAAAGATAC	CAGGCGTTTC	120
CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	160
GCCGCTTACC	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	200
AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	240
GTTGCGGTGTA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	280
CGAACCCCCC	GTTGAGCCCC	ACCGCTGCGC	CTTATCCGGT	320
AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	CACGACTTAT	360
CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	400
GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	440
CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	480
GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	520
TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	560
GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	CGCAGAAAAA	600
AAGGATCT				608

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:27:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCGG	120
CCCTGGACTG	TTGAACGAGG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTTACTG	GCACTTCAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCA	GGCGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCCGTC	TTCCCCTGCA	GGATGAGTAG	TGAGTGCCTC	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCCTAATA	AAATTAAGTT	GCATCATTTT	GTCTGACTAG	440
GTGTCCTCTA	TAATATTATA	AGCTTGATAT	CGAATTCCTT	480
CGGACTTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCA	CCACGGGTAA	TGCTTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGCGC	ATCATATCAA	640
ATGACGCGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTC	680
CTGCAGCCCC	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC	720

GCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTCAG	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACCTAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTTTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	ACTCTAGATG	1320
AGAGAGCAGT	GAGGGAGAGA	CAGAGACTCG	AATTTCCGGA	1360
GCTATTTTCT	TTTTCTTTTC	CGTTTTGTGC	AATTTCACTT	1400
ATGATACCGG	CCAATGCTTG	GTTGCTATTT	TGGAAACTCC	1440
CCTTAGGGGA	TGCCCCCTCA	CTGGCCCTAT	AAAGGGCCAG	1480
CCTGAGCTGC	AGAGGATTCC	TGCAGAGGAT	CAAGACAGCA	1520
CGTGGACCTC	GCACAGCCTC	TCCCACA		1547

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCCG	120
CCCTGGACTG	TTGAACGAGG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTTACTG	GCACTTCAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCA	GGCGGGGATG	280
GGGGAGACCT	GATGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCCGTC	TTCCCCCTGCA	GGATGAGTAG	TGAGTGCCTC	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCCTAATA	AAATTAAGTT	GCATCATTTT	GTCTGACTAG	440
GTGTCCTCTA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCA	CCACGGGTAA	TGCTTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGCGC	ATCATATCAA	640
ATGACGCGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTC	680

CTGCAGCCCCG	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC	720
GCCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTTCT	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACTAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTTTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	CCAACGCGTT	1320
GGATGCATGG	ATGAGGGAAA	GGAGGTAAGA	TCTGTAATGA	1360
ATAAGCAGGA	ACTTTGAAGA	CTCAGTGAAT	CAGTGAGTAA	1400
TAAAGACTCA	GTGACTTCTG	ATCCTGTCCT	AACTGCCACT	1440
CCTTGTTGTC	CCAAGAAAGC	GGCTTCCTGC	TCTCTGAGGA	1480
GGACCCCTTC	CCTGGAAGGT	AAAATAAGG	ATGTCAGCAG	1520
AGAAATTTTT	CCACCATTGG	TGCTTGGTCA	AAGAGGAAAC	1560
TGATGAGCTC	ACTCTAGATG	AGAGAGCAGT	GAGGGAGAGA	1600
CAGAGACTCG	AATTTCCGGA	GCTATTTTCA	TTTTCTTTTC	1640
CGTTTTGTGC	AATTTCACTT	ATGATAACGG	CCAATGCTTG	1680
GTTGCTATTT	TGGAAACTCC	CCTTAGGGGA	TGCCCTCAAA	1720
CTGGCCCTAT	AAAGGGCCAG	CCTGAGCTGC	AGAGGATTCC	1760
TGCAGAGGAT	CAAGACAGCA	CGTGGACCTC	GCACAGCCTC	1800
TCCCACA				1807

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:29:

GGTACCTGCC	ACCATGGCGA	AGGGCGAGGA	ACTGTTCACT	40
GGCGTGGTCC	CAATTCTCGT	GGAAGTGGAT	GGCGATGTGA	80
ATGGGCACAA	ATTTTCTGTC	AGCGGAGAGG	GTGAAGGTGA	120
TGCCACATAC	GGAAAGCTCA	CCCTGAAATT	CATCTGCACC	160
ACTGGAAAGC	TCCCTGTGCC	ATGGCCAACA	TGTTGTCATA	200
CCTTCACCTA	TGGCGTGCAG	TGCTTTTCCA	GATACCCAGA	240
CCATATGAAG	CAGCATGACT	TTTTCAAGAG	CGCCATGCCC	280

GAGGGCTATG	TGCAGGAGAG	AACCATCTTT	TTCAAAGATG	320
ACGGGAACTA	CAAGACCCGC	GCTGAAGTCA	AGTTCGAAGG	360
TGACACCCTG	GTGAATAGAA	TCGAGTTGAA	GGGCATTGAC	400
TTTAAGGAAG	ATGGAAACAT	TCTCGGCCAC	AAGCTGGAAT	440
ACAACTATAA	CTCCACAAAT	GTGTACATCA	TGGCCGACAA	480
GCAAAAGAAT	GGCATCAAGG	TCAACTTCAA	GATCAGACAC	520
AACATTGAGG	ATGGATCCGT	GCAGCTGGCC	GACCATTATC	560
AACAGAACAC	TCCAATCGGC	GACGGCCCTG	TGCTCCTCCC	600
AGACAACCAT	TACCTGTCCA	CCCAGTCTGC	CCTGTCTAAA	640
GATCCCAACG	AAAAGAGAGA	CCACATGGTC	CTGCTGGAGT	680
TTGTGACCGC	TGCTGGGATC	ACACATGGCA	TGGACGAGCT	720
GTACAAGTGA	GCGCCTTAAG	GGCCATATGG	TGAGTGGATG	760
CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	TGTAAGTCAGA	800
GCCCCCGGGC	AGCACAGGCC	AATGCCCCTC	CTTCCCCTGC	840
AGGATGAGTA	GTGAGTGCCT	CTCCTGGCCC	TGGAAGTTGC	880
CACTCCAGTG	CCCACCAGCC	TTGTCTTAAT	AAAAATTAAGT	920
TGCATCATTT	TGTCTGACTA	GGTGTCTCTT	ATAATATTAT	960
AAGCTTGATA	TCGAATTCTT	TCGGACTTTT	GAAAGTGATG	1000
GTGGTGGGGG	AAGGATTCTG	ACCTTCGAAG	TCGATGACGG	1040
CAGATTTAGA	GTCTGCTCCC	TTTGCCCGCT	CGGGAACCCC	1080
ACCACGGGTA	ATGCTTTTAC	TGGCCTGCTC	CCTTATCGGG	1120
AAGCGGGGCG	CATCATATCA	AATGACGCGC	CGCTGTAAAG	1160
TGTTACGTTG	AGAAAGAATT	CCTGCAGCCC	GCCGCGTTGC	1200
TGGCGTTTTT	CCATAGGCTC	CGCCCCCTTG	ACGAGCATCA	1240
CAAAAATCGA	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA	1280
GGACTATAAA	GATACCAGGC	GTTTCCCCCT	GGAAGCTCCC	1320
TCGTGCGCTC	TCCTGTTCCG	ACCCTGCCGC	TTACCGGATA	1360
CCTGTCCGCC	TTTCTCCCTT	CGGGAAGCGT	GGCGCTTTCT	1400
CAATGCTCAC	GCTGTAGGTA	TCTCAGTTCG	GTGTAGGTCTG	1440
TTGCTCCCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA	1480
GCCCGACCGC	TGCGCCTTAT	CCGGTAACTA	TCGTCTTGAG	1520
TCCAACCCGG	TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	1560
CCACTGGTAA	CAGGATTAGC	AGAGCGAGGT	ATGTAGGCGG	1600
TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	CTACGGCTAC	1640
ACTAGAAGGA	CAGTATTTGG	TATCTGCGCT	CTGCTGAAGC	1680
CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG	1720
CAAACAAACC	ACCGCTGGTA	GCGGTGGTTT	TTTTGTTTGC	1760
AAGCAGCAGA	TTACGCGCAG	AAAAAAAGGA	TCTGGGGGGAT	1800
CCGGAGAGCT	CCCAACGCGT	TGGATGCATG	GATGAGGGAA	1840
AGGAGGTAAG	ATCTGTAATG	AATAAGCAGG	AACTTTGAAG	1880
ACTCAGTGAC	TCAGTGAGTA	ATAAAGACTC	AGTGACTTCT	1920
GATCCTGTCC	TAACTGCCAC	TCCTTGTTGT	CCCAAGAAAG	1960
CGGCTTCCTG	CTCTCTGAGG	AGGACCCCTT	CCCTGGAAGG	2000
TAAACTAAG	GATGTCAGCA	GAGAAATTTT	TCCACCATTG	2040
GTGCTTGCTC	AAAGAGGAAA	CTGATGAGCT	CACTCTAGAT	2080
GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	GAATTTCCGG	2120
AGCTATTTCA	GTTTTCTTTT	CCGTTTTGTG	CAATTTCACT	2160
TATGATACCG	GCCAATGCTT	GGTTGCTATT	TTGGAAACTC	2200
CCCTTAGGGG	ATGCCCCCTA	ACTGGCCCTA	TAAAGGGCCA	2240
GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	TCAAGACAGC	2280
ACGTGGACCT	CGCACAGCCT	CTCCCA		2308